

31 YRMFFQAYICILITIGFDDYALQKQDQALOTUPVYAFSFVYLTGLJVIGAFLN 240
11 LVLVLMFTMNAEDBKDEBHEHALLTRNGQAGGGG-----GGSANTDTQASSTAA- 291

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EMBL: AB008579; BAA25436; 1; -.
 EMBL: AF2211798; AAF81418; 1; JOINED.
 EMBL: AF225058; AAB81418; 1; -.
 EMBL: AE051515; AAC29336; 1; -.
 EMBL: AF006624; AKK53367; 1; -.
 EMBL: AB013345; BAM28349; 1; -.
 MGD: MGI:1100509; Kcnk3.
 InterPro: IPR003280; K-channel_pore.
 InterPro: IPR001622; K-channel_pore.
 InterPro: IPR00637; K-channeling.

USE	STANDARD;	PRT;	409 AA.
035163;			
-2001 (Rel. 4.0, Created)			
2001 (Rel. 4.0, Last sequence update)			
2001 (Rel. 4.0, Last annotation update)			
um channel subfamily K member 3 (Acid-sensitive potassium protein (ASK), (TWIK-related acid-sensitive K+ channel), IC TWO-Pore background K ⁺ channel) (CTBAK-1).			
ICUUS (Mouse)			
Xt; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Euteleostomi; Eutharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus. xID=10090;			
E FROM N_A.			
Heart;			
:>8163556; PubMed=9506712;			
Fujita A., Horio Y., Kurachi Y.,			
ig and functional expression of a novel cardiac two-pore			
leak channel (CTBAK-1).;			
Leibig. 82:513-518(1998).			
E FROM N_A.			
Heart;			
:>20287574; PubMed=10748056;			
M., Gallagher P.C., Buck M.E., Butler M.H., Goldstein S.A.;			
block and voltage gating are potassium-dependent in the			
leak channel. <i>Konkai</i> ;			
Chem. 27:15669-16678(2000).			
E OF 4-409 FROM N_A.			
:>9745933; PubMed=9312005;			
F., Lebagne F., Fink M., Reyes R., Heurteaux C., Lazdunski M.;			
a human background K ⁺ channel to sense external pH variations			
physiological pH".			
16:5464-5471(1997).			
CTION: PH-DEPENDENT, VOLTAGE-INSENSITIVE, BACKGROUND POTASSIUM			
IN CHANNEL PROTEIN. RECTIFICATION DIRECTION RESULTS FROM POTASSIUM			
CONCENTRATION ON EITHER SIDE OF THE MEMBRANE. ACTS AS AN			
WARD RECTIFIER WHEN EXTERNAL POTASSIUM CONCENTRATION IS LOW.			
IN EXTERNAL POTASSIUM CONCENTRATION IS HIGH, CURRENT IS INWARD			
SIMILARITY).			
UNIT: HOMODIMER (POTENTIAL).			
ICELLULAR LOCATION: INTEGRAL membrane protein (Potential).			
SUB SPECIFICITY: VERY STRONG EXPRESSION IN HEART, ALSO DETECTED			
KIDNEY, BRAIN, SKIN, TESTIS, LUNG, SKELETAL MUSCLE, SMALL			
TESTICLE, AND STOMACH. NOT DETECTED IN LIVER, THYMUS OR SPLEEN.			
ICELLULAR: INACTIVATED BY BARIUM.			
ICLARITY: BELONGS TO THE TWO PORE DOMAIN FAMILY OF POTASSIUM			
ICNLS.			
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Bioinformatics Institute. There are no restrictions on its			
non-profit institutions as long as its content is in "no			
wave			

InterPro: IPR003021; Task: channel.
 PRF050; Ion trans: 1;
 PRINTS: PR0133; 2P0REK CHANNEL.
 IONIC CHANNEL; TRANSMEMBRANE; Ion transport; Potassium transpo
 GLYCOPROTEIN.
 DOMAIN 1 8 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 9 29 POTENTIAL.
 DOMAIN 78 101 PORE-FORMING 1 (POTENTIAL).
 TRANSMEM 108 128 POTENTIAL.
 DOMAIN 129 158 CYTOPLASMIC (POTENTIAL).
 TRANSMEM 159 179 POTENTIAL.
 DOMAIN 184 207 PORE-FORMING 2 (POTENTIAL).
 TRANSMEM 223 243 POTENTIAL.
 DOMAIN 244 409 CYTOPLASMIC (POTENTIAL).
 CARBOHYD 53 53 N-LINKED GLCNAc (POTENTIAL).
 CONFLICT 4 4 O -> E (IN REF. 3).
 CONFLICT 123 123 V -> I (IN REF. 3).
 SEQUENCE 409 AA: 45068 MM: 35236B011AAC5687 CRC64:
 90.1%; Score: 1840.5; DB 1; Length: 409;
 st Local Similarity 88.5%; Precl. No.: 8; le-138;
 tches 362; Conservative 7; Mismatches 25; Indels 15;
 1 MRKQNYRTIALIVLICFTYLUVGAVIDAESPELIERQRQLRQELQQLRARNI
 1 MRRQNYRTIALIVLICFTYLUVGAVIDAESPELIERQRQLRQELQQLRARNI
 61 ELERVYLRLRKKHAGVORRPGSFYFAITVITIGKHAMSTDGSKVCPY
 61 ELERVYLRLRKKHAGVORRPGSFYFAITVITIGKHAMSTDGSKVCPY
 121 TLVMEQSGERTINTLVRLHRAKGKGLMRRADYMSMANVJGPFCSILCK
 121 TLVMEQSGERTINTLVRLHRAKGKGLMRRADYMSMANVJGPFCSILCK
 181 YEHMFQFOQAXYCITLTIGFGDYVALQDKDQALQTOPOVAFSYVLLGT
 181 YEHMFQFOQAXYCITLTIGFGDYVALQDKDQALQTOPOVAFSYVLLGT
 181 YEHMFQFOQAXYCITLTIGFGDYVALQDKDQALQTOPOVAFSYVLLGT
 241 LVVLREPMTHNAAEDEKDAEHRALLTRNGQAGGGG ----- -GGSATNDTA
 241 LVVLREPMTHNAAEDEKDAEHRALLTRNGQAGGGG ----- -GGSATNDTA
 292 ----- GSGFRNTAYTLEPHFSMNCILWYKREKLYSTIMPTIDRUDSTC
 301 CGVGCVGGSGSGFRNYTAEVLFHPCMCILWYKREKLYSTIMPTIDRUDSTC
 346 SPGGSGGRYKDTSPRCLGSGARSATSSYSVGLHSLSTERGLMKRSSV 394
 361 SPGGGGGRYKDTSPHCPLCGSGTORSATSSVSVSLCHSLAFLRGMLKRSSV 409